Download data link

https://www.ebi.ac.uk/ena/browser/api/xml/SRR2589044?download=true

ls -l : To check written/reading permission of files in a directory

cat filename.ex : To read file

history : To display all commands we are running

Grep tt filename : To search a partern

Grep tt filename > file.txt : to redirect the patter into file.txt

Wc filename : To read line, word and character counts

Wc -l filename: Only the lines in the file

Man wc: to read more about the command

Loop : To run line of code; to run commands repetitively.

For filename in \*.fastq

> do

> head -n 2 ${filename}

>done

…………………………………………. The same as

For filename in \*.fastq; do head -n 2 ${filename}; done ::: one-line command code

for filename in \*.xml;do tail -n 2 ${filename}; done ::::: to read from the tail

Head -n 10 | grep TT SRR097977.fastq :::: To run two commands without for loop.

Nano readme.txt ::: creating file with nano

mv readme.xtx readme.sh :::

current permission: -rwxr-xr-x 1 “We want to change the permission”

chmod +x readme.sh :: to change permission

DARA WRANGLING

download Ecoli\_metadat.xlsx

A command line expressioncut -f2 -d, Ecoli\_metadata\_composite.csv  | sort | uniq | wc -l ::: counting

Getting the raw reads

We will use commands line to download from : <https://www.ebi.ac.uk/ena/browser/home>

mkdir -p ~dc\_workshop/data/untrimmed\_fastq :: creating subsubdirectory

curl -0 downloadable-link ::: to download from the link “https://www.ebi.ac.uk/ena/browser/api/xml/SRR2589044?download=true”